

ID AAZ29722 standard; DNA; 2060 BP.

XX AAZ29722;

XX 27-MAR-2000 (first entry)

XX Human lung specific gene Lng105.

XX Lung Specific Gene; LSG; Lng105; human; diagnostic marker; prognosticate;

XX lung cancer; diagnosis; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX 711..1973

XX CDS

XX /tag= a

XX /product= "LSG Lng105 protein"

XX MO9960160-A1.

XX 25-NOV-1999.

XX 12-MAY-1999; 99WO-US010344.

XX 21-MAY-1998; 98US-0086212P.

XX (DIAD-) DIADEXUS LLC.

XX Yang F, Macina RA, Sun Y;

XX WPI: 2000-116320/10.

XX P-PSDB; AAY44457.

XX A new method for diagnosing, monitoring and staging lung cancer.

XX Claim 6; Page 34-35; 40pp; English.

XX The present sequence is a lung specific gene (LSG) Lng105 from human

XX clone ID 3107312. The LSG has high level of tissue specificity for lungs

XX and is overexpressed in cancerous tissues. The sequence serves as a

XX diagnostic marker for detecting, monitoring, staging and prognosticating

XX lung cancer. The diagnosis involves comparing levels of LSG in samples

XX obtained from patient and normal control

XX Sequence 2060 BP; 458 A; 573 C; 537 G; 492 T; 0 U; 0 Other;

XX Query Match 37.2%; Score 678.4; DB 3; Length 2060;

XX Best Local Similarity 97.8%; Pred. No. 6.4e-197;

XX Matches 704; Conservative 0; Mismatches 1; Indels 15; Gaps 1;

QY 518 CTTGAGAGCTCTCAAAATCTTGGTCATGGATGAAGCCGCGGATCTGATATGGATTT 577

Db 1 CTTGAGAGCTCTCAAAATCTTGGTCATGGATGAAGCCGCGGATCTGATATGGATTT 60

QY 578 TGAGACAGAGGTGACAGATCCTCAAAGTGATTCCTCGAGATCGGAAACATTCCTCTT 637

Db 61 TGAGACAGAGGTGACAGATCCTCAAAGTGATTCCTCGAGATCGGAAACATTCCTCTT 105

QY 638 CTCCTGCCACCATGACCAAGAGGTTCAAAACCTTCAGGACGAGCTCTGAAGAATCCTGT 697

Db

Db 106 CTCTGCCACCATGACCAAGAGGTTCAAAACCTTCAGGAGCAGCTCTGAAGAATCCTGT 165

QY 598 GAAATGTGCCCTTCCCTCTAAATACAGACAGTTGAAAAATTTACAGCAATATTATATTT 757

Db 166 GAAATGTGCCCTTCCCTCTAAATACAGACAGTTGAAAAATTTACAGCAATATTATATTT 225

QY 758 TATTCCCTCTAAATTCAGGATACCTACCTGGTTTATATCTTAATGAATGGCTGAAA 817

Db 226 TATTCCCTCTAAATTCAGGATACCTACCTGGTTTATATCTTAATGAATGGCTGAAA 285

QY 818 CTCCTTTATGATATTCAGCAGCCTGTAATAATACCAGAGAACAGCTTTGCTACTGCG 877

Db 286 CTCCTTTATGATATTCAGCAGCCTGTAATAATACCAGAGAACAGCTTTGCTACTGCG 345

QY 878 AATCTTGGCTTCACTGCCATCCCTCCATGGACAAATGAGTCAGAGTAAGCCCTAGG 937

Db 346 AATCTTGGCTTCACTGCCATCCCTCCATGGACAAATGAGTCAGAGTAAGCCCTAGG 405

QY 938 ATCCCTTAATAAGTTTAAAGGCCAAGGCCGCTTCCATTTCTTAGCAACTGACGTTGCCAG 997

Db 406 ATCCCTTAATAAGTTTAAAGGCCAAGGCCGCTTCCATTTCTTAGCAACTGACGTTGCCAG 465

QY 998 CCGAGTTTGGACATACCTCATGTAGATGGTTGTCAACTTTGACATTCACCCATTC 1057

Db 466 CCGAGTTTGGACATACCTCATGTAGATGGTTGTCAACTTTGACATTCACCCATTC 525

QY 1058 CAAGGATTACATCCATCGAGTAGGTTCGAACAGCTAGAGCTGGGCGCTCCGAAAGGCTAT 1117

Db 526 CAAGGATTACATCCATCGAGTAGGTTCGAACAGCTAGAGCTGGGCGCTCCGAAAGGCTAT 585

QY 1118 TACTTTTGTACACAGTATGATGTGGAATCTTTCAGGCGCATAGAACACTTAATGGGAA 1177

Db 586 TACTTTTGTACACAGTATGATGTGGAATCTTTCAGGCGCATAGAACACTTAATGGGAA 645

QY 1178 GAAACTACAGGTTTTCGAACACAGGATGATGAGTTTATGATGCTGACAGAACGCGTCGC 1237

Db 646 GAAACTACAGGTTTTCGAACACAGGATGATGAGTTTATGATGCTGACAGAACGCGTCGC 705

Sequence Match List  
for SEQ ID NO:12

Mon May 3 08:37:19 2004

Query Match	37.2%;	Score 678.4;	DB 3;	Length 2061;
Best Local Similarity	97.8%;	0; M.8.Se-206;		
Matches 704;	Conservative	1;	Indels 15;	Gaps 1;
518	CTTGAGAGCTCTCAAAATAC	TTGGTCATGGATGAAGCCGACCGAATAC	CTGAATATGATTT	577
1	CTTGAGAGCTCTCAAAATAC	TTGGTCATGGATGAAGCCGACCGAATAC	CTGAATATGATTT	60
578	TGAGACAGAGGTTGACAGATCCT	CAAAATGATTTCTTCGAGATCGGAAAAC	CATTCCTCTT	637
61	TGAGACAGAGGTTGACAG-	-----CCTCGAGATCGGAAAAC	CATTCCTCTT	105
638	CTCTGCCACCATGACCAAGGTT	CAAAAACCTTCAGCGACAGCTCTCGAAGATCCTGT		697
106	CTCTGCCACCAATGACCAAGGTT	CAAAAACCTTCAGCGACAGCTCTCGAAGATCCTGT		165
698	GAATGTGCGGTTTCTCTAAATAC	CAGACAGTTGAAAAATTA	CAGCAATATATATTTT	757
166	GAATGTGCGGTTTCTCTAAATAC	CAGACAGTTGAAAAATTA	CAGCAATATATATTTT	225
758	TATTCCCTCTAAATTC	CAAGATACCTTACCTGGTTTATATTTCTAAATGAATTTGGCTCGAAA		817
226	TATTCCCTCTAAATTC	CAAGATACCTTACCTGGTTTATATTTCTAAATGAATTTGGCTCGAAA		285
818	CTCCTTTATGATATCTCGACGAC	CTGTAAATAAATACCCAGAGAAC	CAGCTTTGCTACTGCG	877
286	CTCCTTTATGATATCTCGACGAC	CTGTAAATAAATACCCAGAGAAC	CAGCTTTGCTACTGCG	345
878	AAATCTTGGGTTCACTGGCCAT	CCCCCTCCATCGACAAATAGT	CAGAGTAAGCGCCTAGG	937
346	AAATCTTGGGTTCACTGGCCAT	CCCCCTCCATCGACAAATAGT	CAGAGTAAGCGCCTAGG	405
938	ATCCCTTAATAGTTTAAGCC	CAAGCCCGTTCCATTTCTTAGCAA	CTGACGTTGCCAG	997
406	ATCCCTTAATAGTTTAAGCC	CAAGCCCGTTCCATTTCTTAGCAA	CTGACGTTGCCAG	465
998	CCGAGGTTTGACATACCT	CACTGATGTTGGTTGTCAACTTTTGACATTTCTTACCCATTC		1057
466	CCGAGGTTTGACATACCT	CACTGATGTTGGTTGTCAACTTTTGACATTTCTTACCCATTC		525
1058	CAAGGATTAATCATCGATGAGT	CGAACAGCTAGAGCTGGCGCTCCGGAAGGCTAT		1117
526	CAAGGATTAATCATCGATGAGT	CGAACAGCTAGAGCTGGCGCTCCGGAAGGCTAT		585
1118	TACTTTTGTCAACAGTATCAT	GTGAACTCTTCCAGCGCATAGAACACTTAATTTGGGAA		1177
586	TACTTTTGTCAACAGTATCAT	GTGAACTCTTCCAGCGCATAGAACACTTAATTTGGGAA		645
1178	GAAACTACCGAGTTTCCAA	CAACAGGATGATGAGTTATGATCTCTGACAGAACCGCGTCGC		1237
646	GAAACTACCGAGTTTCCAA	CAACAGGATGATGAGTTATGATCTCTGACAGAACCGCGTCGC		705

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Sequence Math Listing  
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